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DATA NOTE

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Draft genome sequence of *Bacillus pumilus* strain EZ-C07 isolated from digested agricultural wastes

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Abstract

Objectives: *Bacillus* species, belonging to the family *Bacillaceae*, are rod-shaped aerobic or facultative anaerobic Gram-positive bacteria that can be isolated from various environmental niches. *Bacillus pumilus* strains are resistant to unfavorable conditions such as UV, H_2O_2 and chemical disinfection. Furthermore, *B. pumilus* strains synthesize multifarious important enzymes and can be used in the production of some fermented foods, bioremediation of wastewater systems and biodegradation of environmental contaminants. Hence, investigation at the genomic level is required to understand their ecology, genetics and potential applications.

Data description: In this research, we provide the genomic insights into one *Bacillus* species (EZ-C07) isolated from digested agricultural waste materials. The draft genome of the strain EZ-C07 consists of 3,724,869 bp with 3890 coding sequences and 41.5% G + C content. Based on 16S rRNA gene sequence analysis followed by in silico DNA–DNA hybridization studies, the strain EZ-C07 was identified as *Bacillus pumilus* belonging to the family *Bacillaceae* within the phylum *Firmicutes*. The whole genome shotgun project of *B. pumilus* strain EZ-C07 can be accessed at DDBJ/ENA/GenBank under the Accession QLVI00000000.

Keywords: Poultry manure, Bioreactor, Genome sequencing, *Firmicutes*, *Bacillus pumilus*

Objective

Bacillus species, belonging to the family *Bacillaceae*, are rod-shaped aerobic or facultative anaerobic Gram-positive bacteria that can be isolated from various environments. One of the features of this genus is the ability to form endospores in response to various environmental and nutritional stresses [1, 2]. 16S rRNA gene sequence analysis showed a high level of phylogenetic heterogeneity in the genus *Bacillus*. Members of this genus can produce a wide range of useful pharmaceutical, agricultural and industrial products (such as antibiotics, enzymes, amino acids, sugars) [1–3]. Also, several *Bacillus* strains with strong proteolytic activities displayed the robust survival in the protein-fed anaerobic biogas reactors and finally improved the biogas productivity [4]. The anaerobic digestion of biomass belongs to a more suitable method to utilize various agricultural waste materials [5, 6].

From the array of various *Bacillus* species, *Bacillus pumilus* strains are resistant to unfavorable conditions, including UV, H_2O_2 and chemical disinfection [7, 8]. In addition, based on their abilities to synthesize multifarious enzymes and several other bioactive compounds [9, 10], *B. pumilus* strains can be used in fermented foods production [11], biofertilizers synthesis [12], bioremediation of wastewater systems [13] and biodegradation of environmental contaminants [14]. Moreover, some *B. pumilus* strains were previously isolated from a biogas reactor utilizing abattoir waste [15]. Hence, more investigations at the genomic level are required to understand ecology, genetics and potential applications of *B. pumilus*

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